Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

These amendments introduce no new matter and support for the amendment is replete throughout the specification and claims as originally filed. These amendments are made without prejudice and are not to be construed as abandonment of the previously claimed subject matter, or agreement with any objection or rejection of record.

Listing of Claims:

Claims 1 to 33 (Cancelled).

34. (Currently amended) A method of incorporating a 5-substituted tryptophan unnatural amino acid into a peptide, the method comprising:

preparing a construct comprising a nucleic acid sequence encoding an orthogonal [[mutant tryptophanyl-]]tRNA synthetase (O-~~muTrp~~RS) and comprising at least 90% identity to the sequence of SEQ ID NO: 2, the O-~~muTrp~~RS comprising a proline residue at a position corresponding to position 144 of SEQ ID NO: 2, wherein the O-RS aminoacylates a reference tRNA of SEQ ID No: 3 with a 5-substituted tryptophan analog or 5-hydroxy-L-tryptophan (5-HTTP) when the reference tRNA, 5-substituted tryptophan analog or 5-HTTP, and the O-~~muTrp~~RS are present in a eukaryotic cell;

preparing a construct comprising a nucleic acid sequence encoding an orthogonal tRNA (O-tRNA) comprising: at least 90% identity to SEQ ID NO: 3, wherein the O-tRNA is aminoacylated with the 5-substituted tryptophan analog or 5-HTTP by a reference RS of SEQ ID NO: 2 when the reference RS, 5-substituted tryptophan analog or 5-HTTP, and the O-tRNA are present in eukaryotic cell;

introducing the O-~~muTrp~~RS construct and the O-tRNA construct into the eukaryotic cell; and,

preferentially aminoacylating an expressed O-tRNA with the unnatural amino acid, wherein said aminoacylation is catalyzed by an expressed O-~~muTrp~~RS;

whereby the 5-substituted tryptophan unnatural amino acid or 5-HTTP is incorporated into the peptide in the cell.

35. (Previously presented) The method of claim **34**, wherein the unnatural amino acid is 5-hydroxy-L-tryptophan (5-HTPP).

36. (Original) The method of claim **35**, further comprising applying a voltage to the peptide, thereby reacting the 5-HTPP with a reactive molecule.

37. (Original) The method of claim **36**, wherein reacting comprises cross-linking.

38. (Original) The method of claim **36**, wherein the reactive molecule comprises an unnatural amino acid in another peptide.

39. (Original) The method of claim **34**, further comprising detecting an interaction between the peptide and another peptide.

40. (Original) The method of claim **39**, wherein said detecting comprises fluoroscopy.

41. (Currently amended) The method of claim **34**, wherein the O-~~muTrp~~RS construct comprises a nucleic acid comprising a polynucleotide sequence selected from the group consisting of:

a) a coding polynucleotide sequence selected from the group consisting of SEQ ID NO: 1~~, and a conservative variation thereof~~;

b) a coding polynucleotide sequence that encodes a polypeptide ~~selected from the group consisting~~ of SEQ ID NO: 2~~, and a conservative substitution thereof~~;

c) a polynucleotide sequence which hybridizes under highly stringent conditions over an entire length of a polynucleotide sequence of (a) or (b);

d) a complementary sequence of (a), (b), or (c); and,

e) a Val144Pro mutant of plasmid pEF6-TrpRS (pVal144ProBsTrpRS).

42. (Currently amended) The method of claim **34**, wherein the O-~~muTrp~~RS construct comprises a mutated tryptophanyl-tRNA synthetase peptide sequence mutated at one or more amino acid residues based on structure data of the tryptophanyl-tRNA synthetase or an analogous aminoacyl-tRNA synthetase.

43. (Original) The method of claim **42**, wherein the mutated tryptophanyl-tRNA synthetase comprises a *Bacillus* tryptophanyl-tRNA synthetase mutated at Val144.

44. (Previously presented) The method of claim **34**, wherein the O-tRNA construct comprises a polynucleotide sequence selected from the group consisting of: SEQ ID NO: 3, and a complementary polynucleotide sequence thereof.

45. (Original) The method of claim **34**, wherein said preparing the O-tRNA construct comprises inclusion of one or more tRNA flanking sequences that functionally interact with an RNA polymerase of the cell.

46. (Original) The method of claim **34**, wherein the O-tRNA construct comprises an A box eukaryotic transcriptional control element.

47. (Currently amended) The method of claim **34**, further comprising mutating the ~~a prokaryotic~~ O-tRNA sequence to include a functional A box eukaryotic transcriptional control element.

48. (Original) The method of claim **47**, wherein said mutating comprises site directed mutagenesis.

49. (Currently amended) The method of claim **34**, wherein the O-tRNA construct or O-~~muTrp~~RS construct comprises: a reporter tag or a purification tag.

50. (Currently amended) The method of claim **34**, wherein the O-~~muTrp~~RS encoding construct and the O-tRNA encoding construct comprise the same construct.

51. (Original) The method of claim **34**, wherein the O-tRNA recognizes a selector codon in a nucleic acid sequence encoding the peptide, thereby incorporating the unnatural amino acid into the peptide.

52. (Original) The method of claim **34**, further comprising transfecting a nucleic acid encoding the peptide into the cell.

53. (Previously presented) The method of claim **52**, wherein the cell comprises a mammalian cell.

54. (Currently amended) The method of claim **34**, further comprising expressing the O-~~muTrp~~RS construct or the O-tRNA construct.

55. (Currently amended) The method of claim **54**, further comprising purifying expressed O-~~muTrp~~RS or expressed O-tRNA.

Claims 56 to 62 (Cancelled).

63. (Currently amended) The method of claim **34**, wherein the O-~~muTrp~~RS comprises at least 95% identity to SEQ ID NO: 2.

64. (Currently amended) The method of claim **34**, wherein the O-~~muTrp~~RS comprises at least 98% identity to SEQ ID NO: 2.

65. (Currently amended) The method of claim **34**, further comprising mutating and screening a nucleic acid encoding the amino acid sequence of SEQ ID NO: 2 to obtain the O-~~muTrp~~RS.

66. (Currently amended) The method of claim **34**, wherein the O-~~muTrp~~RS comprises with two adjacent binding pockets separated by an a-helix peptide consisting of Asp at a position corresponding to position 140, Ile at a position corresponding to position 141, Val at a position corresponding to position 142, Pro at a position corresponding to position 143, Gly at a position corresponding to position 145.

67. (Currently amended) The method of claim **34**, wherein the O-~~muTrp~~RS comprises Ser at a position corresponding to position 7, His at a position corresponding to position 44, and Asp at a position corresponding to position 133.

68. (Previously presented) The method of claim **46**, wherein the A box eukaryotic transcriptional control element comprises: G at a position corresponding to position 7, G at a position corresponding to position 9, or U at a position corresponding to position 11.

69. (Previously presented) The method of claim **34**, wherein the O-tRNA comprises at least 95% identity to the sequence of SEQ ID NO: 3.